

5' TGG CGC TTG CCG AGT GAT TCT CCT CGA ATA CCT CCT GCC GGC GCG GAG ACA CCG  
 10 19 28 37 46 55  
 GGG CGG GGG TCC TGC CGC AAC TAC CTC CCT TCC TCC TCT CCC CCG CCC CCG GAG  
 64 73 82 91 100 109  
 CCT TCA TCC TTC CCT TCC CCC CCC ACC TCG AGG GGC GGG CCT GGT TCC CGG GAC  
 118 127 136 145 154 163  
 ACC ATG TCG GAC TCT GAG GAG AGC CAG GAC CGG CAA CTG AAA ATC GTC GTG  
 172 181 190 199 208 217  
 M S D S E E E S Q D R Q L K I V V  
 CTG GGG GAC GNN GCC TCC GGG AAG ACC TCC TTA ACT ACG TGT TTT GCT CAA GAA  
 226 235 244 253 262 271  
 L G D X A S G K T S L T T C F A Q E  
 ACT TTT GGG AAA CAG TAC AAA CAA ACT ATA GGA CTG GAT TTC TTT TTG AGA AGG  
 280 289 298 307 316 325  
 T F G K Q Y K Q T I G L D F F L R R  
 ATA ACA TTG CCA GGA AAC TTG AAT GTT ACC CTT CAA ATT TGG GAT ATA GGA GGG  
 334 343 352 361 370 379  
 I T L P G N L N V T L Q I W D I G G  
 CAG ACA ATA GGA GGC AAA ATG TTG GAT AAA TAT ATC TAT GGA GCA CAG GGA GTC  
 388 397 406 415 424 433  
 Q T I G G K M L D K Y I Y G A Q G V  
 CTC TTG GTA TAT GAT ATT ACA AAT TAT CAA AGC TTT GAG AAT TTA GAA GAT TGG  
 442 451 460 469 478 487  
 L L V Y D I T N Y Q S F E N L E D W  
 TAT ACT GTG GTG AAG AAA GTG AGC NAG GAG TCA GAA ACT CAG CCA CTG GTT GCC  
 496 505 514 523 532 541  
 Y T V V K K V S X E S E T Q P L V A  
 TTG GTA GGC AAT AAA ATT GAT TTG GAG CAT ATG CGA ACA ATA AAA CCT GAA AAA  
 550 559 568 577 586 595  
 L V G N K I D L E H M R T I K P E K  
 CAC TTA CGG TTT TGC CAG GAA AAT GGT TTT AGT AGC CAC TTT GTC TCA GCC AAG  
 604 613 622 631 640 649  
 H L R F C Q E N G F S S H F V S A K  
 ACA GGA GAC TCT GTC TTC CTG TGC TTT CAG AAA GTT GCT GCT GAA ATC CTT GGG  
 658 667 676 685 694 703  
 T G D S V F L C F Q K V A A E I L G

FIGURE 1A

0988974.11901

1. *Chlorophyll a* (Chl *a*)  
 2. *Chlorophyll b* (Chl *b*)  
 3. *Carotenoids* (Car)  
 4. *Phenolics* (Phen)  
 5. *Proteins* (Pro)  
 6. *Lipids* (Lip)  
 7. *Starch* (Starch)  
 8. *Cellulose* (Cellulose)  
 9. *Hemicellulose* (Hemicellulose)  
 10. *Pectin* (Pectin)  
 11. *Other* (Other)

ATC	AAA	712	TTA	AAC	AAN	721	NAG	CAG	AAW	730	TRG	MAC	AGT	739	CAC	AGW	GGG	748	GTG	GTG	AAG	757	GSA
I	K	L	N	X	X	Q	X	X	X	X	X	S	H	X	G	V	V	K	X				
GRT	ATT	766	GTA	AAC	TAC	775	AAC	CAG	GAA	784	CCT	ATG	TCA	793	AGG	ACT	KTT	802	AAC	CCT	CCT	811	AGA
X	I	V	N	Y	N	Q	E	P	M	S	R	T	X	N	P	P	R						
AGC	TCT	820	ATG	TGT	GCA	829	GTT	CAG	TGA	838	GCG	CAT	TTT	847	NCT	TTT	GTN	856	TTG	ATA	GTT	865	CTG
S	S	M	C	A	V	Q																	
GCT	GCC	874	CTT	CAA	CTC	883	TGG	GTG	GGN	892	CCC	NAG	GGC	901	TTC	TAG	GAC	910	TTG	TTT	T	3'	

[illegible]

FIGURE 1B

05307-11901

FIGURE 2A

Docket No.: PF-0183-2 DIV  
Inventors: Hillman et al.  
Title: RAB PROTEINS  
Serial No.: To Be Assigned

712 721 730 739 748 757  
AGC CTC TGA CCT TGG CCA GCA CCA CCT GCC CCC ACT GGC TTT TTG GTG CCC CTT  
S L  
766 775 784 793 802 811  
GTC CCC ACT TCA GCC CCA GGA CCT TTC CTT GCC CTT TGG TTC CAG ATA TCA GAC  
820 829 838 847  
TGT TCC CTG TTC ACA GCA CCC TCA GGG TCT TAA GGT 3'

FIGURE 2B

0988974-111901

5' CTG TGA TGA AAC ACT TTT CCC GTG TCG TTT GAG TGC ATC TTC TCA ACA ACC CTA  
11 20 29 38 47 56  
GGA GGG TTC TTG AAG CTT TTG AGA TTA ACA ATG GCA GGA AAA TCA TCA CTT TTT  
65 74 83 92 101 110  
M A G K S S L F  
AAA GTA ATT CTC CTT GGA GAT GGT GGA GTT GGG AAG AGT TCA CTT ATG AAC AGA  
119 128 137 146 155 164  
K V I L L G D G G V G K S S L M N R  
TAT GTA ACT AAT AAG TTT GAT ACC CAG CTC TTC CAT ACA ATA GGT GTG GAA TTT  
173 182 191 200 209 218  
Y V T N K F D T Q L F H T I G V E F  
TTA AAT AAA GAT TTG GAA GTG GAT GGA CAT TTT GTT ACC ATG CAG ATT TGG GAC  
227 236 245 254 263 272  
L N K D L E V D G H F V T M Q I W D  
ACG GCA GGT CAG GAG CGA TTC CGA AGC CTG AGG ACA CCA TTT TAC AGA GGT TCT  
281 290 299 308 317 326  
T A G Q E R F R S L R T P F Y R G S  
GAC TGC TGC CTG CTT ACT TTT AGT GTC GAT GAT TCA CAA AGC TTC CAG AAC TTA  
335 344 353 362 371 380  
D C C L L T F S V D D S Q S F Q N L  
AGT AAC TGG AAG AAA GAA TTC ATA TAT TAT GCA GAT GTG AAA GAG CCT GAG AGC  
389 398 407 416 425 434  
S N W K K E F I Y Y A D V K E P E S  
TTT CCT TTT GTG ATT CTG GGT AAC AAG ATT GAC ATA AGC GAA CGG CAG GTG TCT  
443 452 461 470 479 488  
F P F V I L G N K I D I S E R Q V S  
ACA GAA GAA GCC CAA GCT TGG TGC AGG GAC AAC GGC GAC TAT CCT TAT TTT GAA  
497 506 515 524 533 542  
T E E A Q A W C R D N G D Y P Y F E  
ACA AGT GCA AAA GAT GCC ACA AAT GTG GCA GCA GCC TTT GAG GAA GCG GTT CGA  
551 560 569 578 587 596  
T S A K D A T N V A A A F E E A V R  
AGA GTT CTT GCT ACC GAG GAT AGG TCA GAT CAT TTG ATT CAG ACA GAC ACA GTC  
605 614 623 632 641 650  
R V L A T E D R S D H L I Q T D T V

FIGURE 3A

09988974-111901

AAT	CTT	659		668		677		686		695		704					
N	L	H	R	K	P	K	P	S	S	S	C	C					
		713		722		731		740		749		758					
TGA	TGC	ATT	CTA	ACC	AAC	TCA	CAC	ATA	TAC	ACA	AAA	TCA	ACA	TGG	GGA	TGG	AGA
		767		776		785		794		803		812					
AGA	GAA	TTA	GCG	TTT	GCA	GCA	GTG	TAT	CAT	CTA	CTA	ATA	AAA	TTA	AAC	TAA	TGT
		821		830		839		848		857		866					
TGC	TGC	TTC	ATT	AGT	TGG	TGG	GAG	AAG	GGA	CAC	ATC	CAC	TCT	TGG	AGG	AAT	ATA
		875		884		893		902		911		920					
TTT	ACT	CAA	TAA	TGG	CAC	CTT	ACA	TTT	ATA	AAT	TGT	AAC	AGT	TGT	CTA	ATA	ACG
		929		938		947		956		965		974					
TTT	CTT	TAA	TTT	AAA	TAT	GTA	AGT	TGC	AGA	GCT	AAT	AAA	TGA	AAT	GAC	CAA	GAC
		983		992		1001		1010		1019		1028					
TTT	AAT	TAT	AAT	AAA	AAT	AAG	AAA	CTT	GAC	TAT	TCT	AGA	AGT	TAT	ACT	TGG	ATT
		1037		1046		1055		1064		1073		1082					
TTT	TCC	TGG	GAA	AAT	GGA	GAA	CTA	CTT	TTT	ATA	TGT	GTA	TGT	TTT	TAT	GCA	ATT
		1091		1100		1109		1118		1127		1136					
AGC	ATT	GTA	TTC	TTG	GTT	CAG	GGA	AAT	ACT	TTC	CTA	AAG	CAA	TAA	TGT	TAG	ATA
		1145		1154		1163		1172									
TTA	AAG	ATT	AAA	ATC	TAA	TGT	AAA	AAA	AAA	AAA	AAA	AAA	AAA	3'			

FIGURE 3B

0988974-71904

1	M S D S E E E S Q D R Q - - - - L K I V V L G D X A S G K T	SEQ ID NO-1
1	M S D S E E E S Q D R Q - - - - L K I V V L G D G T S G K T	GI 1154901
1	M R X K M G N G T E E D Y N F V F K V V L I G E S G V G K T	SEQ ID NO-3
1	M G N - - - - - - - - - - L F K V I L L G D G G V G K S	GI 436001
1	M A G K S S - - - - - - - - - - L F K V I L L G D G G V G K S	SEQ ID NO-5
1	M A G K S S - - - - - - - - - - L F K V I L L G D G G V G K S	GI 486830
27	S L T T C F A Q E T F G K Q Y K Q T I G L D F F L R R I T L	SEQ ID NO-1
27	S L A T C F A Q E T F G K Q Y K Q T I G L D F F L R R I T L	GI 1154901
31	N L L S R F T R N E F S H D S R T T I G V E F S T R T V M L	SEQ ID NO-3
27	N L L S R F T R N E F S H D S R T T I G V E F S T R T V L L	GI 436001
22	S L M N R Y V T N K F D T Q L F H T I G V E F L N K D L E V	SEQ ID NO-5
22	S L M N R Y V T N K F D T Q L F H T I G V E F L N K D L E V	GI 486830
57	P G N L N V T L Q I W D I G G Q T I G G K M L D K Y I Y G A	SEQ ID NO-1
57	P G N L N V T L Q I W D I G G Q T I G G K M L D K Y I Y G A	GI 1154901
61	G T A A - V K A Q I W D T A G L E R Y R A I T S A Y Y R G A	SEQ ID NO-3
57	G T A A - V K A Q I W D T A G L E R Y R A I T S A Y Y R G A	GI 436001
52	D G H F - V T M Q I W D T A G Q E R F R S L R T P F Y R G S	SEQ ID NO-5
52	D G H F - V T M Q I W D T A G Q E R F R S L R T P F Y R G S	GI 486830
87	Q G V L L V Y D I T N Y Q S F E N L E D W Y T V V K K V S X	SEQ ID NO-1
87	Q G I L L V Y D I T N Y Q S F E N L E D W Y S V V K T V S E	GI 1154901
90	V G A L L V F D L T K H Q T Y A V V E R W L K E L - - Y D H	SEQ ID NO-3
86	V G A L L V F D L T K H Q T Y A V V E R W L K E L - - Y D H	GI 436001
81	D C C L L T F S V D D S Q S F Q N L S N W K K E F I Y Y A D	SEQ ID NO-5
81	D C C L L T F S V D D S Q S F Q N L S N W K K E F I Y Y A D	GI 486830
117	E S E T Q P L V - A L V G N K I D L E H M R T I K P E K H L	SEQ ID NO-1
117	E S E T Q P L V - A L V G N K I D L E H M R T V K P D K H L	GI 1154901
118	A E A - - T I V V M L V G N K S D L S Q G R E V P T E E A R	SEQ ID NO-3
114	A E A - - T I V V M L V G N K S D L S Q A R E V P T E E A R	GI 436001
111	V K E P E S F P F V I L G N K I D I S E - R Q V S T E E A Q	SEQ ID NO-5
111	V K E P E S F P F V I L G N K I D I S E - R Q V S T E E A Q	GI 486830
146	R F C Q E N G F S S H F - V S A K T G D S V F L C F Q K V A	SEQ ID NO-1
146	R F C Q E N G F S S H F - V S A K T G D S V F L C F Q K V A	GI 1154901
146	M F A E N N G - L L F L E T S A L D S T N V E L A F E T V L	SEQ ID NO-3
142	M F A E N N G - L L F L E T S A L D S T N V E L A F E T V L	GI 436001
140	A W C R D N G D Y P Y F E T S A K D A T N V A A A F E E A V	SEQ ID NO-5
140	A W C R D N G D Y P Y F E T S A K D A T N V A A A F E E A V	GI 486830
175	A E I L G I K L N X X Q X X X S H X G V V K X X I V N Y N Q	SEQ ID NO-1
175	A E I L G I K L N K A E I E Q S Q R - V V K A D I V N Y N Q	GI 1154901
175	K E I F - - - - - A K V S K Q R Q N S I R T N A I T L G S	SEQ ID NO-3
171	K E I F - - - - - A K V S K Q I Q N S P R S N A I A L G S	GI 436001
170	R R V L - - - - - A T - E D R S D H L I Q T D T V N L - -	SEQ ID NO-5
170	R R V L - - - - - A T - E D R S D H L I Q T D T V S L - -	GI 486830
205	E P M S R T X N P P R S S M C A V Q	SEQ ID NO-1
204	E P M S R T V N P P R S S M C A V Q	GI 1154901
199	A Q X G Q E P G P G E K R A C C I S L	SEQ ID NO-3
195	A Q A G O E P G P G Q K R A C C I N L	GI 436001
191	- - - - - H R K P K P S S S C C	SEQ ID NO-5
191	- - - - - H R K P K P S S S C C	GI 486830

FIGURE 4

0988974-11901

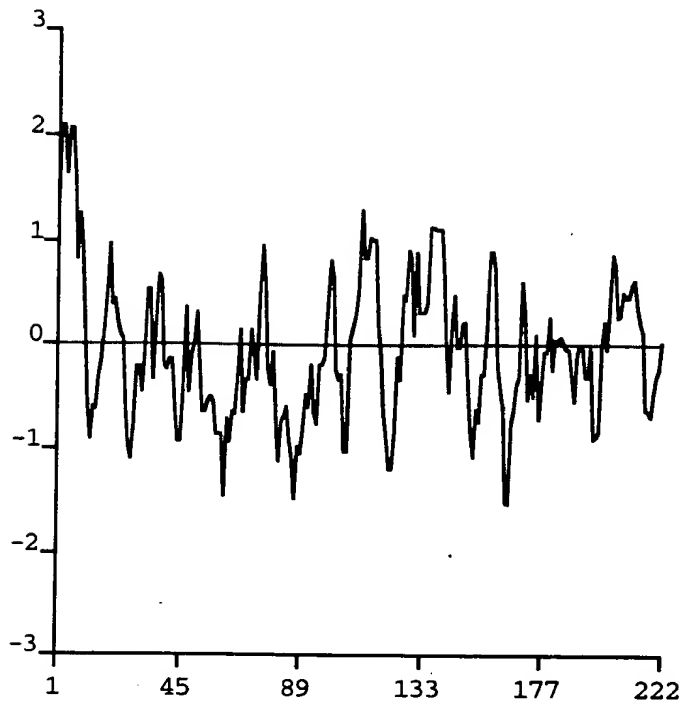
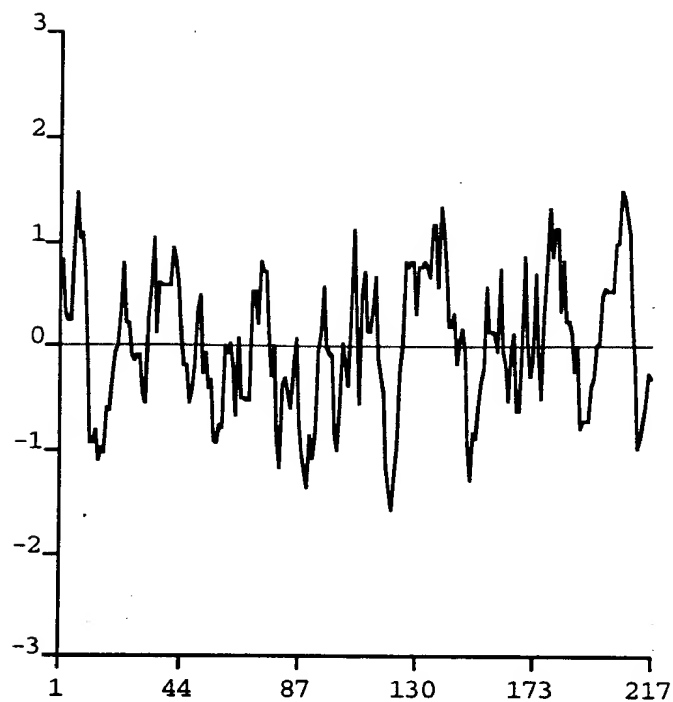


FIGURE 5





0988974-11901

FIGURE 6

0988974-11901

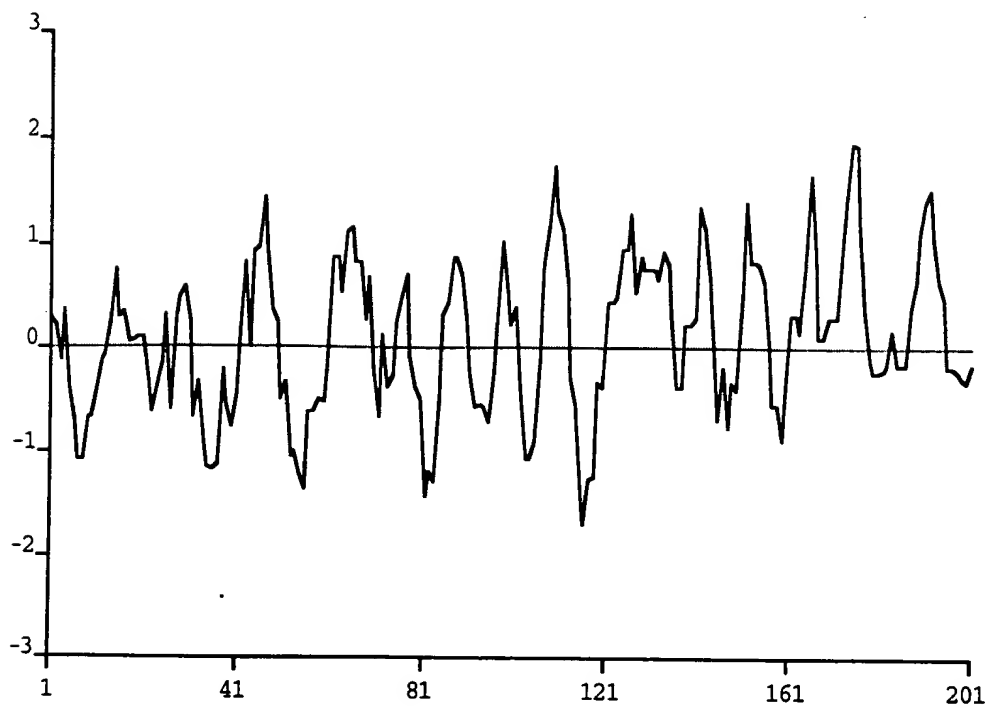


FIGURE 7

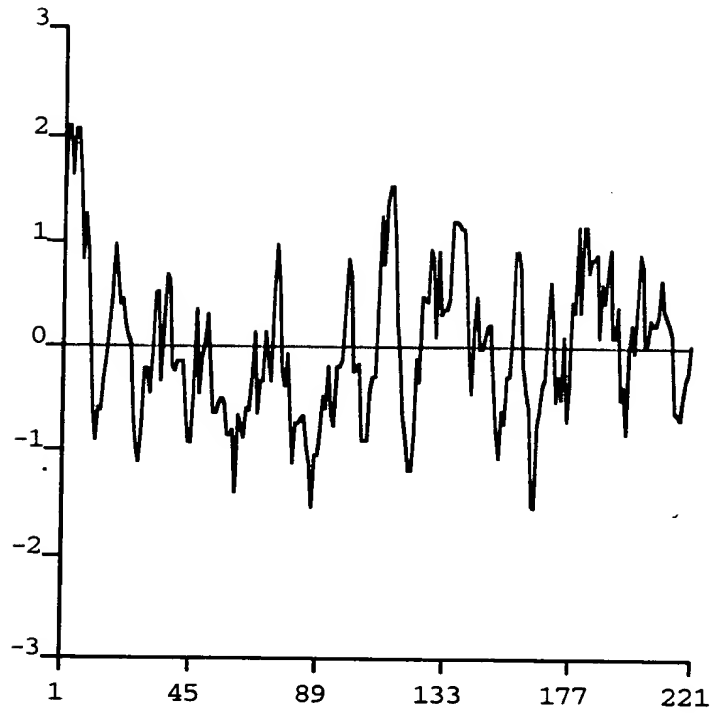


FIGURE 8